

FIGURE 1A

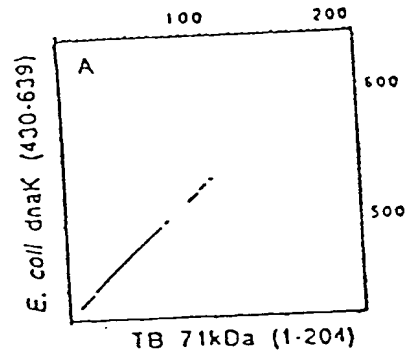
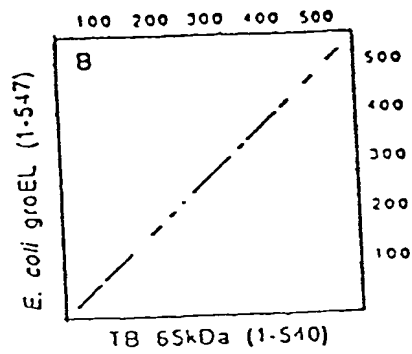


FIGURE 1B



	1	10	20	30	40	50	60	70
UMP1	MLRLPTVFRQMRPVSRVLAPHLTRAYAKDVKFGADARALMLQGVDLLADAVAVTMGPKGRTVIEEQSWGS							
GROEL	-----MA-----AKDVKFGNDARVKMLRGVNVVLADAVKVTLGPKGRNVVLDKSFGA							
	71	80	90	100	110	120	130	140
HUMP1	PKVTKDGVTVAKSIDLKDKYKNIGAKLVQDVANNTNEEAGDGTATVLAQAIITEGLKAVAAGMNPMDL							
GROEL	PTITKDGVSVAEIEPEDKFENMGAQMVKEVASKANDAAGDGTATVLAQAIITEGLKAVAAGMNPMDL							
	141	150	160	170	180	190	200	210
HUMP1	RRGVMLAVDAVIAELKKQSKPVTTPEDIAQVATISANGDKEIGNIISDAMKKVGRKGVITVKDGKTLNDE							
GROEL	KRGIDKAVTAAVEELKALSVPCSDSKAIAQVGTISANSDETGVGLIAEAMDKVGKEGVITVEDGTGLQDE							
	211	220	230	240	250	260	270	280
HUMP1	LEIIEGMKFDRGYISPYFINTSKGQKCEFDAYVLLSEKKISSIQSIVPALEIANAHKPLVITAEVDVG							
GROEL	LDVVEGMQFDRGYLSPYFINKPETGAVELESFILLADKKISNIREMLPVLEAVAKAGKPLLIIEADVEG							
	281	290	300	310	320	330	340	350
HUMP1	EALSTLVNRLKVGLQVVAVKAPGFGDNRNKQLKDMAIATGGAVFGEEGLTNLEDVQPHDLGKVGEVIV							
GROEL	EALATAVVNTIRGIVKVAAVKAPGFGDRRKAMLQDIATLTGGTVISEE-IGMELEKATLEDLGQAKRVVI							
	351	360	370	380	390	400	410	420
HUMP1	TKDDAMLLKKGDKAQIEKRIQEIIEQLDVTTSEYEKEKLNRLAKLSGDGVAVLKVGGTSDVEVNEKKDF							
GROEL	NKDTTTIIDGVGEEAAIQGRVAQIROQIEEATSDYDREKLQERVAKLAGGVAVIKVGAATEVEMKEKKA							
	421	430	440	450	460	470	480	490
HUMP1	VTDALNATRAAVEEGIVLGGGCALLRCIPALDSLTPANEDQKIGIEIIRTLKIPAMTIKNAGVEGSL							
GROEL	VEDALHATRAAVEEGVVAGGGVALIRVASKLADLRGQNEQQNVVSSSL-RAMEAPLRQIVLNCGEPSV							
	491	500	510	520	530	540	550	56
HUMP1	VEKIMQSSSEVGYDAMAGDFVNMVEKGIIDPTKVVRTALLDAAGVASLLTTAEVVVTEIPKEEKDPGMS							
GROEL	ANTVKGGDGNVGYNAATEEYGNMIDMGILDPTKVTRSAALQYAASVAGLNIITECMVTDLPKND-AADLG							
	561	570						
HUMP1	MGGMG--GMGGGMF							
GROEL	AGGMGGMGGMGGM-							

Total score = 4667, 5 breaks  
 276 identities out of 545 possible matches between residues

25 random runs  
 Alignment score = 65.34 SD Standard deviation = 18.94 Mean = 3429.48

	1	10	20	30	40	50	60	70
HUMP1	MLRLPTVFRQMRPVSRVLAPHLTRAYAKDVKFGADARALMLQGV	DL	LADAVAVTMGPKGRTV	IEQSWGS				
HL65K	M-----			AKTIAYDEEARRGLERGLNSLADAVKVTLGPKGRNVVLEKKWGA				
	71	80	90	100	110	120	130	140
HUMP1	PKVTKDGVTVAKSIDLKDKYKNIGAKLVQDVANNTNEEAGDGT	TT	TATV	LARSIAKEGF	EKISKGANPVEI			
HL65K	PTITNDGV	SI	AK	EIELED	PEYKIG	AELVKEVAKKTDDVAGDGT	TT	TATVLAQALVKEGLRNVAAGANPLGL
	141	150	160	170	180	190	200	210
HUMP1	RRGVMLAVDAVIAELKKQSKPVTTPEEIAQVATISANGDKEI	GN	IISDAMKKVGRKGVITVKDGKTLNDE					
HL65K	KRGIEKAVDKVTETLLKDAKEVETKEQIAATAAISA-GDQ	SIGDLIAEAMD	KVGN	EGVITVEESNT	TFGLQ			
	211	220	230	240	250	260	270	280
HUMP1	LEIIIEGMKFDRGYISPYFINTSKGQKCEFQDAYVLLSEKK	ISSIQSIVPALEIAN	AHRKPLVIIAEDVDG					
HL65K	LELTEGMRFDKGYISGYFVTD	AERQ	EAVLE	EPYILLVSSKVSTVKDLLP	LEKVIQAGKSLIIAEDVEG			
	281	290	300	310	320	330	340	350
HUMP1	EALSTLVNLRLKVGLQVVAVKAPGFGDNRKNQLKDMAI	ATGGAVFGEEGLTLNLEDVQPHDLGKVGEVIV						
HL65K	EALSTLVN	KIRGTFKSVAVKAPGFGDRRKAM	LQDMAILTGAQVISEE-VGLTLENTDLSLLGKARKVVM					
	351	360	370	380	390	400	410	420
HUMP1	TKDDAMLLKGKGDKAQIEKRIQEIIIEQLDVT	TSEYEKEKLN	ERLAKLS	DGVAVLXVGGTSDVEVNEKKDR				
HL65K	TKDETTIVEGAGDTDAI	AGRVAQIRTEIENS	SDSDYDREKLQERLAKLAGGVAVIKAGAATEVELKERKHS					
	421	430	440	450	460	470	480	490
HUMP1	VTDALNATRAAVEEGIVLGGGCALLRCIPALDSLTPANEDQK	IGIEIIKRTLKIPAMTI	AKNAGVEGSLI					
HL65K	IEDAVRNAKA	AVEEGIVAGGGVTLLQAAPALDKL	LTGDEAT-GANIVKVALEAPLKQIAFNSGMEPGV					
	491	500	510	520	530	540	550	560
HUMP1	VEKIMQSSSEVGYDAMAGDFVNMVEKGIIDPTKVV	RTALLDAAGVASLLTTAEVVVTEIPKEEKDPGMG						
HL65K	AEKVRNLSVGHGLNAATGEYEDLLKAGVADPVKV	TR	SALQNAASIAGLFTT-EAVVADKPEKTAAPASD					
	561	570						
HUMP1	MGGMG	GGMG	GGMG	GGMG				
HL65K	TGGMG	G-MD---						

Total score = 4552, 7 breaks  
 255 identities out of 540 possible matches between residues

25 random runs  
 Alignment score = 47.73 SD Standard deviation = 23.86 Mean = 3413.15

FIGURE 4

```

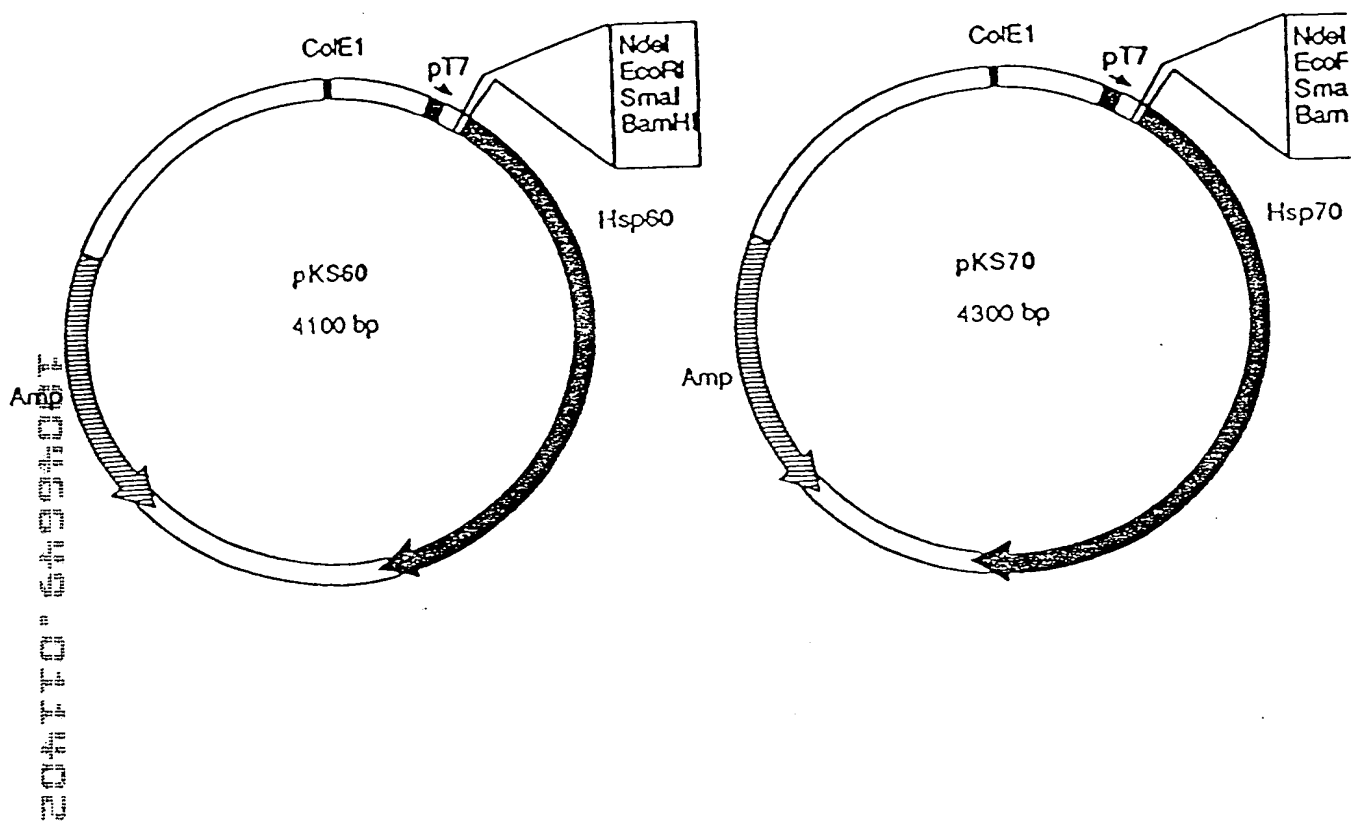
1          10          20          30          40          50          60          70
HUMP1      MLRLPTVFRQMRPVSRVLAPHLTRAYAKDVKFGADARALMLQGVDLLADAVAVTMGPKGRTVIIIEQSWGS
TB65K      M-----AKTIAYDEEARRGLERGLNALADAVKVTLGPKGRNVVLEKKWGA
71          80          90          100         110         120         130         140
HUMP1      PKVTKDGVTVAKSIDLDKDYKNIGAKLVQDVANNTNEEAGDGTATVLRSLIAKEGFEKISKGANPVEI
TB65K      PTITNDGVSLAKEIELEDPEYKIGAEVLVKEVAKKTDVAGDGTATVLAQALRKEGLRNVAAGANPLGI
141         150         160         170         180         190         200         210
HUMP1      RRGVMLAVDAVIAELKKQSKPVTTPEEIAQVATISANGDKEIGNIISDAMKKVGRKGVITVKDGKTLNDE
TB65K      KRGIEKAVEKVTETLLKGAKEVETKEQIAATAAISA-GDQSIGDLIAEAMDKVGNEGVITVEESNTFGLK
211         220         230         240         250         260         270         280
HUMP1      LEIIEGMKFDRGYISPYFINTSKGQKCEFQDAYVLLSEKKISSIQSIVPALEIANAHKPLVIIAEDVDG
TB65K      LELTEGMRFDKGYISGYFVTDPERQEAVLEDPYILLVSSKVSTVKDLLPLEKVIAGKPLIIAEDVEG
281         290         300         310         320         330         340         350
HUMP1      EALSTLVNLRLKVGLQVVAVKAPGFGDNRKNQLKDMAIATGGAVFGEEGLTLNLEDVQPHDLGKVGEVI
TB65K      EALSTLVVNKIRGTFKSVAVKAPGFGDRRKAMLQDMAILTGGQVISEE-VGLTLENADLSLLGKARKVV
351         360         370         380         390         400         410         420
HUMP1      TKDDAMLLKGKGDKAQIEKRIQEIIIEQLDVTTSSEYEKEXLNERLAKLSDGVAVLVKVGGTSDVEVNEKKD
TB65K      TKDETTIVEGAGDTDAIAGRVAQIRQEIENSDDSDYDREKLQERLAKLAGGVAVIKAGAATEVELKERKH
421         430         440         450         460         470         480         490
HUMP1      VTDALNATRAAVEEGIVLGGGCALLRCIPALDSLTSPANEDQKIGIEIIKRTLKIPAMTIAKNAGVEGSI
TB65K      IEDAVRNAKAAVEEGIVAGGGVTLQAAPTLDLKL-LEGDEATGANIVKVALEAPLKQIAFNSGLEPGV
491         500         510         520         530         540         550         560
HUMP1      VEKIMQSSSEVGYDAMAGDFVNMVEKGIIDPTKVVRTALLDAAGVASLLTTAEVVVTEIPKEEKDPGMG
TB65K      AEKVRNLPAGHGLNAQTGVYEDLLAAGVADPVKVTRSAIQNAASIAGLFLTTEAVVADKPEKEKASVP
561         570
HUMP1      MGGMGGMGGMGGMF
TB65K      ----GGDMGGMDF

```

Total score = 4560, 5 breaks  
257 identities out of 540 possible matches between residues

25 random runs  
Alignment score - 49.36 SD Standard deviation - 23.23 Mean - 3413.15

Figure 5



204470" 64994007

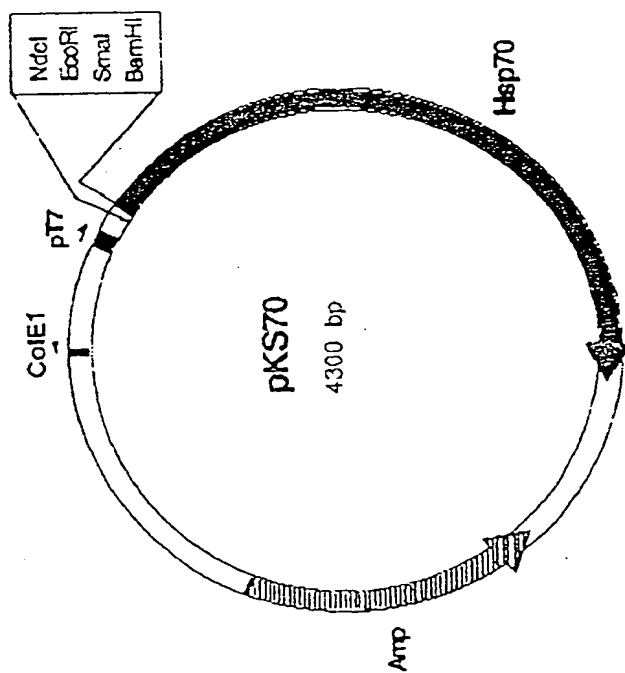
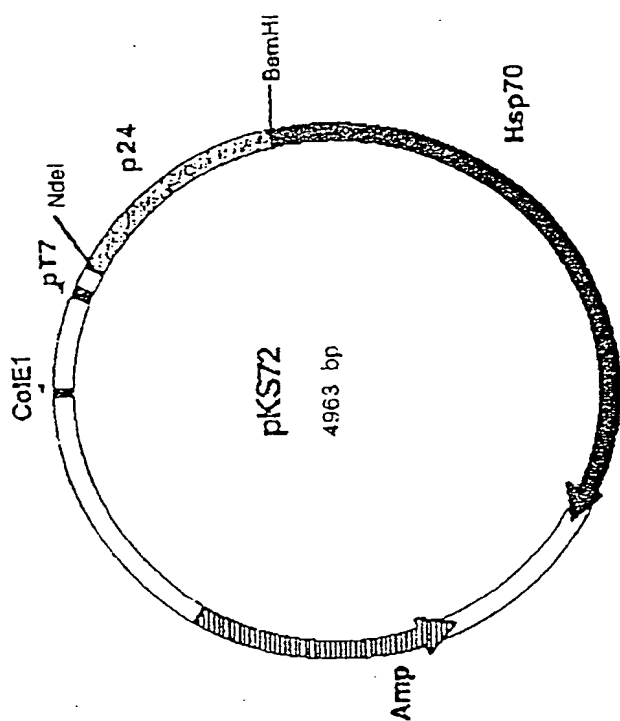


FIGURE 6

2010-03-01

### anti-p24 antibody titer (3 weeks after boost)

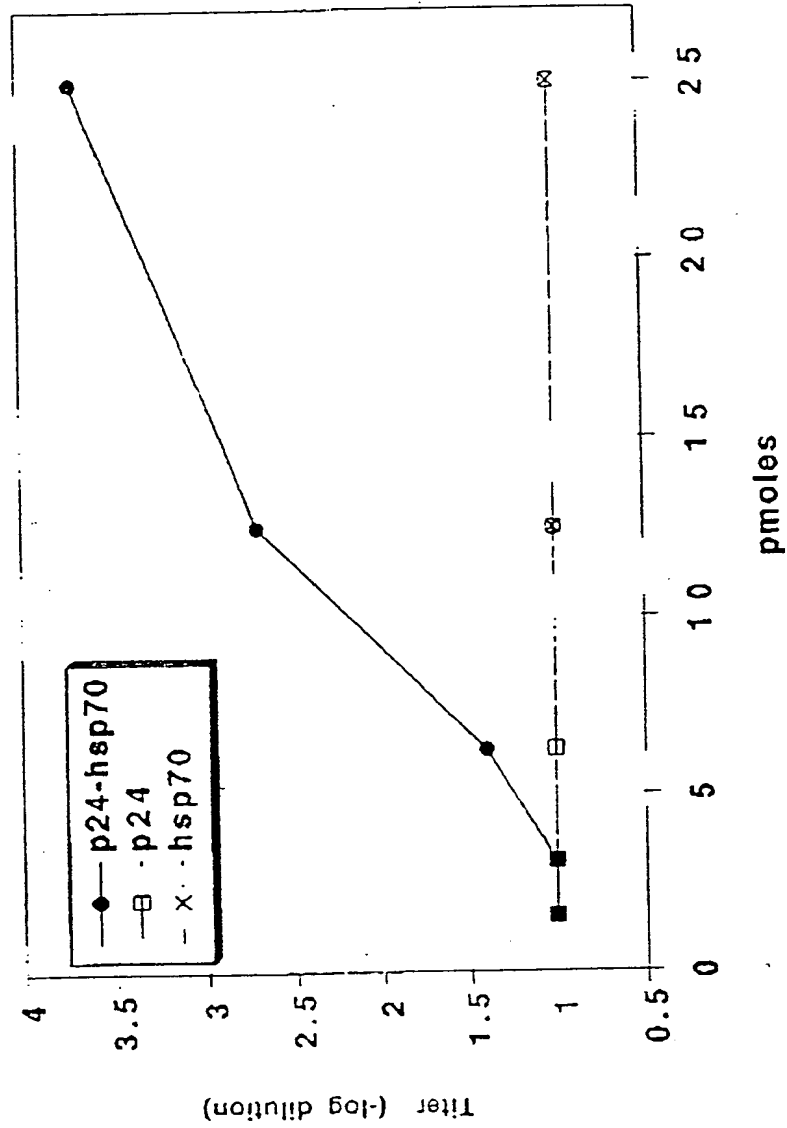


FIGURE 7